RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____10/019,048 B_____

Source: _____JFW/6_____

Date Processed by STIC: _____08/01/2006_____

ENTERED

RAW SEQUENCE LISTING   DATE: 08/01/2006
PATENT APPLICATION: US/10/019,048B   TIME: 10:10:49

Input Set : **A:\00930032.APP**
Output Set: **N:\CRF4\08012006\J019048B.raw**

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 3 <110> APPLICANT: HEINZ, ERNST
 4         GIRKE, THOMAS
 5         SCHEFFLER, JODI
 6         SILVA, OSWALDO DA COSTA E
 8 <120> TITLE OF INVENTION: PLANTS EXPRESSING DELTA-6-DESATURASE GENES,
 9         PUFAS-CONTAINING OILS FROM THESE PLANTS, AND A PROCESS
10         FOR THE PREPARATION OF UNSATURATED FATTY ACIDS
12 <130> FILE REFERENCE: 0093/000032
14 <140> CURRENT APPLICATION NUMBER: 10/019,048B
15 <141> CURRENT FILING DATE: 2001-12-27
17 <150> PRIOR APPLICATION NUMBER: DE 10030976.3
18 <151> PRIOR FILING DATE: 2000-06-03
20 <150> PRIOR APPLICATION NUMBER: 09/347,531
21 <151> PRIOR FILING DATE: 1999-07-06
23 <160> NUMBER OF SEQ ID NOS: 13
25 <170> SOFTWARE: PatentIn Ver. 3.3
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 2012
29 <212> TYPE: DNA
30 <213> ORGANISM: Physcomitrella patens
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (319)..(1896)
36 <400> SEQUENCE: 1
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41 tacctccggg ttttggagcg ggcaaactct gttgcggctc ggaaggctat aggttcggca 180
43 ggagactgtt gattttatgt cgggggcatt gccattgtgg agagcggggg agactcagga 240
45 tctgtgagtg tgcgtgcagc gccccgactg ccgcagagcg tctgtgtatg acgaggttgt 300
47 tgtggagcgg cttttgaa atg gta ttc gcg ggc ggt gga ctt cag cag ggc    351
48                    Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly
49                     1               5                  10
51 tct ctc gaa gaa aac atc gac gtc gag cac att gcc agt atg tct ctc    399
52 Ser Leu Glu Glu Asn Ile Asp Val Glu His Ile Ala Ser Met Ser Leu
53              15              20                  25
55 ttc agc gac ttc ttc agt tat gtg tct tca act gtt ggt tcg tgg agc    447
56 Phe Ser Asp Phe Phe Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser
57          30              35                  40
59 gta cac agt ata caa cct ttg aag cgc ctg acg agt aag aag cgt gtt    495
60 Val His Ser Ile Gln Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val
61      45              50                  55
63 tcg gaa agc gct gcc gtg caa tgt ata tca gct gaa gtt cag aga aat    543
64 Ser Glu Ser Ala Ala Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn
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65  60                    65               70                    75
67  tcg agt acc cag gga act gcg gag gca ctc gca gaa tca gtc gtg aag   591
68  Ser Ser Thr Gln Gly Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys
69                    80               85                    90
71  ccc acg aga cga agg tca tct cag tgg aag aag tcg aca cac ccc cta   639
72  Pro Thr Arg Arg Arg Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu
73                    95               100                   105
75  tca gaa gta gca gta cac aac aag cca agc gat tgc tgg att gtt gta   687
76  Ser Glu Val Ala Val His Asn Lys Pro Ser Asp Cys Trp Ile Val Val
77              110               115                   120
79  aaa aac aag gtg tat gat gtt tcc aat ttt gcg gac gag cat ccc gga   735
80  Lys Asn Lys Val Tyr Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly
81        125               130                   135
83  gga tca gtt att agt act tat ttt gga cga gac ggc aca gat gtt ttc   783
84  Gly Ser Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe
85  140               145                   150                   155
87  tct agt ttt cat gca gct tct aca tgg aaa att ctt caa gac ttt tac   831
88  Ser Ser Phe His Ala Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr
89                    160               165                   170
91  att ggt gac gtg gag agg gtg gag ccg act cca gag ctg ctg aaa gat   879
92  Ile Gly Asp Val Glu Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp
93                    175               180                   185
95  ttc cga gaa atg aga gct ctt ttc ctg agg gag caa ctt ttc aaa agt   927
96  Phe Arg Glu Met Arg Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser
97              190               195                   200
99  tcg aaa ttg tac tat gtt atg aag ctg ctc acg aat gtt gct att ttt   975
100 Ser Lys Leu Tyr Tyr Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe
101       205               210                   215
103 gct gcg agc att gca ata ata tgt tgg agc aag act att tca gcg gtt   1023
104 Ala Ala Ser Ile Ala Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val
105 220               225                   230                   235
107 ttg gct tca gct tgt atg atg gct ctg tgt ttc caa cag tgc gga tgg   1071
108 Leu Ala Ser Ala Cys Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp
109                   240               245                   250
111 cta tcc cat gat ttt ctc cac aat cag gtg ttt gag aca cgc tgg ctt   1119
112 Leu Ser His Asp Phe Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu
113             255               260                   265
115 aat gaa gtt gtc ggg tat gtg atc ggc aac gcc gtt ctg ggg ttt agt   1167
116 Asn Glu Val Val Gly Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser
117             270               275                   280
119 aca ggg tgg tgg aag gag aag cat aac ctt cat cat gct gct cca aat   1215
120 Thr Gly Trp Trp Lys Glu Lys His Asn Leu His His Ala Ala Pro Asn
121       285               290                   295
123 gaa tgc gat cag act tac caa cca att gat gaa gat att gat act ctc   1263
124 Glu Cys Asp Gln Thr Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu
125 300               305                   310                   315
127 ccc ctc att gcc tgg agc aag gac ata ctg gcc aca gtt gag aat aag   1311
128 Pro Leu Ile Ala Trp Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys
129             320               325                   330
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131 aca ttc ttg cga atc ctc caa tac cag cat ctg ttc ttc atg ggt ctg    1359
132 Thr Phe Leu Arg Ile Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu
133             335             340             345
135 tta ttt ttc gcc cgt ggt agt tgg ctc ttt tgg agc tgg aga tat acc    1407
136 Leu Phe Phe Ala Arg Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr
137         350             355             360
139 tct aca gca gtg ctc tca cct gtc gac agg ttg ttg gag aag gga act     1455
140 Ser Thr Ala Val Leu Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr
141     365             370                 375
143 gtt ctg ttt cac tac ttt tgg ttc gtc ggg aca gcg tgc tat ctt ctc    1503
144 Val Leu Phe His Tyr Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu
145 380             385             390                 395
147 cct ggt tgg aag cca tta gta tgg atg gcg gtg act gag ctc atg tcc    1551
148 Pro Gly Trp Lys Pro Leu Val Trp Met Ala Val Thr Glu Leu Met Ser
149             400             405             410
151 ggc atg ctg ctg ggc ttt gta ttt gta ctt agc cac aat ggg atg gag    1599
152 Gly Met Leu Leu Gly Phe Val Phe Val Leu Ser His Asn Gly Met Glu
153             415             420             425
155 gtt tat aat tcg tct aaa gaa ttc gtg agt gca cag atc gta tcc aca    1647
156 Val Tyr Asn Ser Ser Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr
157         430             435             440
159 cgg gat atc aaa gga aac ata ttc aac gac tgg ttc act ggt ggc ctt    1695
160 Arg Asp Ile Lys Gly Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu
161     445             450             455
163 aac agg caa ata gag cat cat ctt ttc cca aca atg ccc agg cat aat    1743
164 Asn Arg Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn
165 460             465             470                 475
167 tta aac aaa ata gca cct aga gtg gag gtg ttc tgt aag aaa cac ggt    1791
168 Leu Asn Lys Ile Ala Pro Arg Val Glu Val Phe Cys Lys Lys His Gly
169             480             485             490
171 ctg gtg tac gaa gac gta tct att gct acc ggc act tgc aag gtt ttg    1839
172 Leu Val Tyr Glu Asp Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu
173             495             500             505
175 aaa gca ttg aag gaa gtc gcg gag gct gcg gca gag cag cat gct acc    1887
176 Lys Ala Leu Lys Glu Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr
177         510             515             520
179 acc agt taa cagtctttgg aaagcttggc aattgatctt tattctccac      1936
180 Thr Ser
181         525
183 ggcagttgct tgtttgtttt ggggtgaatg accgaatgta ctggcatcca ttcttctgta 1996
185 gccatcaatt ttgaac                                              2012
188 <210> SEQ ID NO: 2
189 <211> LENGTH: 525
190 <212> TYPE: PRT
191 <213> ORGANISM: Physcomitrella patens
193 <400> SEQUENCE: 2
194 Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly Ser Leu Glu Glu Asn
195  1               5               10              15
197 Ile Asp Val Glu His Ile Ala Ser Met Ser Leu Phe Ser Asp Phe Phe
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198              20              25              30
200 Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln
201         35              40              45
203 Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala
204         50              55              60
206 Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly
207 65              70              75              80
209 Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg
210              85              90              95
212 Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val
213             100             105             110
215 His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr
216         115             120             125
218 Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser
219         130             135             140
221 Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala
222 145             150             155             160
224 Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu
225             165             170             175
227 Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg
228             180             185             190
230 Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr
231         195             200             205
233 Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala
234         210             215             220
236 Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys
237 225             230             235             240
239 Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe
240             245             250             255
242 Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly
243             260             265             270
245 Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys
246         275             280             285
248 Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr
249         290             295             300
251 Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp
252 305             310             315             320
254 Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile
255             325             330             335
257 Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg
258             340             345             350
260 Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu
261         355             360             365
263 Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr
264         370             375             380
266 Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro
267 385             390             395             400
269 Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly
270             405             410             415
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272 Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser
273             420             425             430
275 Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly
276         435             440             445
278 Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu
279     450             455             460
281 His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala
282 465             470             475                 480
284 Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp
285             485             490             495
287 Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu
288         500             505             510
290 Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser
291         515             520             525
295 <210> SEQ ID NO: 3
296 <211> LENGTH: 6
297 <212> TYPE: PRT
298 <213> ORGANISM: Artificial Sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
302       peptide
304 <400> SEQUENCE: 3
305 Ser Glu Lys Asp Glu Leu
306     1               5
309 <210> SEQ ID NO: 4
310 <211> LENGTH: 20
311 <212> TYPE: DNA
312 <213> ORGANISM: Artificial Sequence
314 <220> FEATURE:
315 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
316       oligonucleotide
318 <220> FEATURE:
319 <221> NAME/KEY: modified_base
320 <222> LOCATION: (15)
321 <223> OTHER INFORMATION: Inosine
323 <400> SEQUENCE: 4
W--> 324 tggtggaart ggamncayaa      .                              20
327 <210> SEQ ID NO: 5
328 <211> LENGTH: 17
329 <212> TYPE: DNA
330 <213> ORGANISM: Artificial Sequence
332 <220> FEATURE:
333 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
334       oligonucleotide
336 <220> FEATURE:
337 <221> NAME/KEY: modified_base
338 <222> LOCATION: (6)
339 <223> OTHER INFORMATION: a, c, g, or t
341 <400> SEQUENCE: 5
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/01/2006
PATENT APPLICATION: US/10/019,048B   TIME: 10:10:50

Input Set : A:\00930032.APP
Output Set: N:\CRF4\08012006\J019048B.raw

Please Note:
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.**

Seq#:4; N Pos. 15
Seq#:5; N Pos. 6

VERIFICATION SUMMARY   DATE: 08/01/2006
PATENT APPLICATION: **US/10/019,048B**   TIME: 10:10:50

Input Set : **A:\00930032.APP**
Output Set: **N:\CRF4\08012006\J019048B.raw**

L:324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0